SEQUENCE LISTING

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      Douglas C. Saffran
      Stephen C. Mitchell

<120> NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
   EXPRESSED IN HUMAN CANCERS AND USES THEREOF

<130> 129.17-US-I1

<140> 09/455,486
<141> 1999-12-06

<150> 09/323,873
<151> 1999-06-01

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<170> FastSEQ for Windows Version 4.0

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    Met Glu Ser Arg Lys Asp Ile Thr Asn Gln Glu Glu Leu Trp Lys
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atg aag cct agg aga aat tta gaa gaa gac gat tat ttg cat aag gac   156
Met Lys Pro Arg Arg Asn Leu Glu Glu Asp Asp Tyr Leu His Lys Asp
                 20   25   30

acg gga gag acc agc atg cta aaa aga cct gtg ctt ttg cat ttg cac   204
Thr Gly Glu Thr Ser Met Leu Lys Arg Pro Val Leu Leu His Leu His
             35   40   45

caa aca gcc cat gct gat gaa ttt gac tgc cct tca gaa ctt cag cac   252
Gln Thr Ala His Ala Asp Glu Phe Asp Cys Pro Ser Glu Leu Gln His
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aca cag gaa ctc ttt cca cag tgg cac ttg cca att aaa ata gct gct   300
Thr Gln Glu Leu Phe Pro Gln Trp His Leu Pro Ile Lys Ile Ala Ala
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att ata gca tct ctg act ttt ctt tac act ctt ctg agg gaa gta att   348

1

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Ile Ile Ala Ser Leu Thr Phe Leu Tyr Thr Leu Leu Arg Glu Val Ile
 80                   85                  90                  95

cac cct tta gca act tcc cat caa caa tat ttt tat aaa att cca atc      396
His Pro Leu Ala Thr Ser His Gln Gln Tyr Phe Tyr Lys Ile Pro Ile
                100                 105                 110

ctg gtc atc aac aaa gtc ttg cca atg gtt tcc atc act ctc ttg gca      444
Leu Val Ile Asn Lys Val Leu Pro Met Val Ser Ile Thr Leu Leu Ala
                115                 120                 125

ttg gtt tac ctg cca ggt gtg ata gca gca att gtc caa ctt cat aat      492
Leu Val Tyr Leu Pro Gly Val Ile Ala Ala Ile Val Gln Leu His Asn
                130                 135                 140

gga acc aag tat aag aag ttt cca cat tgg ttg gat aag tgg atg tta      540
Gly Thr Lys Tyr Lys Lys Phe Pro His Trp Leu Asp Lys Trp Met Leu
        145                 150                 155

aca aga aag cag ttt ggg ctt ctc agt ttc ttt ttt gct gta ctg cat      588
Thr Arg Lys Gln Phe Gly Leu Leu Ser Phe Phe Phe Ala Val Leu His
160                 165                 170                 175

gca att tat agt ctg tct tac cca atg agg cga tcc tac aga tac aag      636
Ala Ile Tyr Ser Leu Ser Tyr Pro Met Arg Arg Ser Tyr Arg Tyr Lys
                180                 185                 190

ttg cta aac tgg gca tat caa cag gtc caa caa aat aaa gaa gat gcc      684
Leu Leu Asn Trp Ala Tyr Gln Gln Val Gln Gln Asn Lys Glu Asp Ala
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tgg att gag cat gat gtt tgg aga atg gag att tat gtg tct ctg gga      732
Trp Ile Glu His Asp Val Trp Arg Met Glu Ile Tyr Val Ser Leu Gly
        210                 215                 220

att gtg gga ttg gca ata ctg gct ctg ttg gct gtg aca tct att cca      780
Ile Val Gly Leu Ala Ile Leu Ala Leu Leu Ala Val Thr Ser Ile Pro
        225                 230                 235

tct gtg agt gac tct ttg aca tgg aga gaa ttt cac tat att cag agc      828
Ser Val Ser Asp Ser Leu Thr Trp Arg Glu Phe His Tyr Ile Gln Ser
240                 245                 250                 255

aag cta gga att gtt tcc ctt cta ctg ggc aca ata cac gca ttg att      876
Lys Leu Gly Ile Val Ser Leu Leu Leu Gly Thr Ile His Ala Leu Ile
                260                 265                 270

ttt gcc tgg aat aag tgg ata gat ata aaa caa ttt gta tgg tat aca      924
Phe Ala Trp Asn Lys Trp Ile Asp Ile Lys Gln Phe Val Trp Tyr Thr
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cct cca act ttt atg ata gct gtt ttc ctt cca att gtt gtc ctg ata      972
Pro Pro Thr Phe Met Ile Ala Val Phe Leu Pro Ile Val Val Leu Ile
                290                 295                 300

ttt aaa agc ata cta ttc ctg cca tgc ttg agg aag aag ata ctg aag     1020
Phe Lys Ser Ile Leu Phe Leu Pro Cys Leu Arg Lys Lys Ile Leu Lys
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2

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att aga cat ggt tgg gaa gac gtc acc aaa att aac aaa act gag ata      1068
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320                 325                 330                 335

tgt tcc cag ttg tag aattactgtt tacacacatt tttgttcaat attgatatat    1123
Cys Ser Gln Leu  *


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<213> Homo sapiens

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Gly Glu Thr Ser Met Leu Lys Arg Pro Val Leu Leu His Leu His Gln
        35                  40                  45
Thr Ala His Ala Asp Glu Phe Asp Cys Pro Ser Glu Leu Gln His Thr
    50                  55                  60
Gln Glu Leu Phe Pro Gln Trp His Leu Pro Ile Lys Ile Ala Ala Ile
65                  70                  75                  80
Ile Ala Ser Leu Thr Phe Leu Tyr Thr Leu Leu Arg Glu Val Ile His
                85                  90                  95
Pro Leu Ala Thr Ser His Gln Gln Tyr Phe Tyr Lys Ile Pro Ile Leu
                100                 105                 110
Val Ile Asn Lys Val Leu Pro Met Val Ser Ile Thr Leu Leu Ala Leu
                115                 120                 125
Val Tyr Leu Pro Gly Val Ile Ala Ala Ile Val Gln Leu His Asn Gly
        130                 135                 140
Thr Lys Tyr Lys Lys Phe Pro His Trp Leu Asp Lys Trp Met Leu Thr
145                 150                 155                 160
Arg Lys Gln Phe Gly Leu Leu Ser Phe Phe Phe Ala Val Leu His Ala
                165                 170                 175
Ile Tyr Ser Leu Ser Tyr Pro Met Arg Arg Ser Tyr Arg Tyr Lys Leu
            180                 185                 190
Leu Asn Trp Ala Tyr Gln Gln Val Gln Gln Asn Lys Glu Asp Ala Trp
        195                 200                 205
Ile Glu His Asp Val Trp Arg Met Glu Ile Tyr Val Ser Leu Gly Ile
    210                 215                 220
Val Gly Leu Ala Ile Leu Ala Leu Leu Ala Val Thr Ser Ile Pro Ser
225                 230                 235                 240
Val Ser Asp Ser Leu Thr Trp Arg Glu Phe His Tyr Ile Gln Ser Lys
                245                 250                 255
Leu Gly Ile Val Ser Leu Leu Leu Gly Thr Ile His Ala Leu Ile Phe
            260                 265                 270
Ala Trp Asn Lys Trp Ile Asp Ile Lys Gln Phe Val Trp Tyr Thr Pro
        275                 280                 285
Pro Thr Phe Met Ile Ala Val Phe Leu Pro Ile Val Val Leu Ile Phe
    290                 295                 300
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Lys Ser Ile Leu Phe Leu Pro Cys Leu Arg Lys Lys Ile Leu Lys Ile
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Ser Gln Leu

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<212> DNA
<213> Homo sapiens

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accaagaaga actttggaaa atgaagccta ggagaaattt agaagaagac gattatttgc   180
ataaggacac gggagagacc agcatgctaa aaagacctgt gcttttgcat ttgcaccaaa   240
cagcccatgc tgatgaattt gactgccctt cagaacttca gcacacacag gaactctttc   300
cacagtggca cttgccaatt aaaatagctg ctattatagc atctctgact tttctttaca   360
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4

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cccctggctg ttcgcgatcc agcttgggta ggcggggaag cagctggagt gcgaccgcca    180
cggcagccac cctgcaaccg ccagtcggag gtgcagtccg taggccctgg cccccgggtg    240
ggcccttggg gagtcggcgc cgctcccgag gagctgcaag gctcgcccct gcccggcgtg    300
gagggcgcgg ggggcgcgga ggatattctt ggtgatcttg aagtgtccg tatc atg      357
                                                              Met
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gaa tca atc tct atg atg gga agc cct aag agc ctt agt gaa act tgt    405
Glu Ser Ile Ser Met Met Gly Ser Pro Lys Ser Leu Ser Glu Thr Cys
              5                  10                  15
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tta cct aat ggc ata aat ggt atc aaa gat gca agg aag gtc act gta    453
Leu Pro Asn Gly Ile Asn Gly Ile Lys Asp Ala Arg Lys Val Thr Val
          20                  25                  30
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ggt gtg att gga agt gga gat ttt gcc aaa tcc ttg acc att cga ctt    501
Gly Val Ile Gly Ser Gly Asp Phe Ala Lys Ser Leu Thr Ile Arg Leu
      35                  40                  45
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5

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Ile Arg Cys Gly Tyr His Val Val Ile Gly Ser Arg Asn Pro Lys Phe
 50              55                  60                  65

gct tct gaa ttt ttt cct cat gtg gta gat gtc act cat cat gaa gat          597
Ala Ser Glu Phe Phe Pro His Val Val Asp Val Thr His His Glu Asp
                70                  75                  80

gct ctc aca aaa aca aat ata ata ttt gtt gct ata cac aga gaa cat          645
Ala Leu Thr Lys Thr Asn Ile Ile Phe Val Ala Ile His Arg Glu His
                85                  90                  95

tat acc tcc ctg tgg gac ctg aga cat ctg ctt gtg ggt aaa atc ctg          693
Tyr Thr Ser Leu Trp Asp Leu Arg His Leu Leu Val Gly Lys Ile Leu
            100                 105                 110

att gat gtg agc aat aac atg agg ata aac cag tac cca gaa tcc aat          741
Ile Asp Val Ser Asn Asn Met Arg Ile Asn Gln Tyr Pro Glu Ser Asn
    115                 120                 125

gct gaa tat ttg gct tca tta ttc cca gat tct ttg att gtc aaa gga          789
Ala Glu Tyr Leu Ala Ser Leu Phe Pro Asp Ser Leu Ile Val Lys Gly
130                 135                 140                 145

ttt aat gtt gtc tca gct tgg gca ctt cag tta gga cct aag gat gcc          837
Phe Asn Val Val Ser Ala Trp Ala Leu Gln Leu Gly Pro Lys Asp Ala
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agc cgg cag gtt tat ata tgc agc aac aat att caa gcg cga caa cag          885
Ser Arg Gln Val Tyr Ile Cys Ser Asn Asn Ile Gln Ala Arg Gln Gln
                165                 170                 175

gtt att gaa ctt gcc cgc cag ttg aat ttc att ccc att gac ttg gga          933
Val Ile Glu Leu Ala Arg Gln Leu Asn Phe Ile Pro Ile Asp Leu Gly
            180                 185                 190

tcc tta tca tca gcc aga gag att gaa aat tta ccc cta cga ctc ttt          981
Ser Leu Ser Ser Ala Arg Glu Ile Glu Asn Leu Pro Leu Arg Leu Phe
    195                 200                 205

act ctc tgg aga ggg cca gtg gtg gta gct ata agc ttg gcc aca ttt         1029
Thr Leu Trp Arg Gly Pro Val Val Val Ala Ile Ser Leu Ala Thr Phe
210                 215                 220                 225

ttt ttc ctt tat tcc ttt gtc aga gat gtg att cat cca tat gct aga         1077
Phe Phe Leu Tyr Ser Phe Val Arg Asp Val Ile His Pro Tyr Ala Arg
                230                 235                 240

aac caa cag agt gac ttt tac aaa att cct ata gag att gtg aat aaa         1125
Asn Gln Gln Ser Asp Phe Tyr Lys Ile Pro Ile Glu Ile Val Asn Lys
                245                 250                 255

acc tta cct ata gtt gcc att act ttg ctc tcc cta gta tac ctt gca         1173
Thr Leu Pro Ile Val Ala Ile Thr Leu Leu Ser Leu Val Tyr Leu Ala
                260                 265                 270
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6

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ggt ctt ctg gca gct gct tat caa ctt tat tac ggc acc aag tat agg        1221
Gly Leu Leu Ala Ala Ala Tyr Gln Leu Tyr Tyr Gly Thr Lys Tyr Arg
    275             280             285

aga ttt cca cct tgg ttg gaa acc tgg tta cag tgt aga aaa cag ctt        1269
Arg Phe Pro Pro Trp Leu Glu Thr Trp Leu Gln Cys Arg Lys Gln Leu
290             295             300             305

gga tta cta agt ttt ttc ttc gct atg gtc cat gtt gcc tac agc ctc        1317
Gly Leu Leu Ser Phe Phe Phe Ala Met Val His Val Ala Tyr Ser Leu
            310             315             320

tgc tta ccg atg aga agg tca gag aga tat ttg ttt ctc aac atg gct        1365
Cys Leu Pro Met Arg Arg Ser Glu Arg Tyr Leu Phe Leu Asn Met Ala
            325             330             335

tat cag cag gtt cat gca aat att gaa aac tct tgg aat gag gaa gaa        1413
Tyr Gln Gln Val His Ala Asn Ile Glu Asn Ser Trp Asn Glu Glu Glu
            340             345             350

gtt tgg aga att gaa atg tat atc tcc ttt ggc ata atg agc ctt ggc        1461
Val Trp Arg Ile Glu Met Tyr Ile Ser Phe Gly Ile Met Ser Leu Gly
    355             360             365

tta ctt tcc ctc ctg gca gtc act tct atc cct tca gtg agc aat gct        1509
Leu Leu Ser Leu Leu Ala Val Thr Ser Ile Pro Ser Val Ser Asn Ala
370             375             380             385

tta aac tgg aga gaa ttc agt ttt att cag tct aca ctt gga tat gtc       .1557
Leu Asn Trp Arg Glu Phe Ser Phe Ile Gln Ser Thr Leu Gly Tyr Val
            390             395             400

gct ctg ctc ata agt act ttc cat gtt tta att tat gga tgg aaa cga        1605
Ala Leu Leu Ile Ser Thr Phe His Val Leu Ile Tyr Gly Trp Lys Arg
            405             410             415

gct ttt gag gaa gag tac tac aga ttt tat aca cca cca aac ttt gtt        1653
Ala Phe Glu Glu Glu Tyr Tyr Arg Phe Tyr Thr Pro Pro Asn Phe Val
            420             425             430

ctt gct ctt gtt ttg ccc tca att gta att ctg gat ctt ttg cag ctt        1701
Leu Ala Leu Val Leu Pro Ser Ile Val Ile Leu Asp Leu Leu Gln Leu
            435             440             445

tgc aga tac cca gac tga gctggaactg gaatttgtct tcctattgac              1749
Cys Arg Tyr Pro Asp *
450


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catgtgactg agtgttggcc agtgagatga agtctcctca aaggaaggca gcatgtgtcc     1869
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actacttccc tacttccact gcttttcctg catttaagcc attgtaaatc tgggtgtgtt     2049
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gcaattcaca ttaaaattga ttttccattg tcaattagtt atactcattt tcctgccttg     2229
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7

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ttggtaatta ctaaaactct gtaatctcca aaatattgct atcaaattac acaccatgtt    2349
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<212> PRT
<213> Homo sapiens

<400> 6

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Val Gly Val Ile Gly Ser Gly Asp Phe Ala Lys Ser Leu Thr Ile Arg
         35                  40                  45
Leu Ile Arg Cys Gly Tyr His Val Val Ile Gly Ser Arg Asn Pro Lys
     50                  55                  60
Phe Ala Ser Glu Phe Phe Pro His Val Val Asp Val Thr His His Glu
65                  70                  75                  80
Asp Ala Leu Thr Lys Thr Asn Ile Ile Phe Val Ala Ile His Arg Glu
                 85                  90                  95
His Tyr Thr Ser Leu Trp Asp Leu Arg His Leu Leu Val Gly Lys Ile
            100                 105                 110
Leu Ile Asp Val Ser Asn Asn Met Arg Ile Asn Gln Tyr Pro Glu Ser
            115                 120                 125
Asn Ala Glu Tyr Leu Ala Ser Leu Phe Pro Asp Ser Leu Ile Val Lys
            130                 135                 140
Gly Phe Asn Val Val Ser Ala Trp Ala Leu Gln Leu Gly Pro Lys Asp
145                 150                 155                 160
Ala Ser Arg Gln Val Tyr Ile Cys Ser Asn Asn Ile Gln Ala Arg Gln
                165                 170                 175
Gln Val Ile Glu Leu Ala Arg Gln Leu Asn Phe Ile Pro Ile Asp Leu
            180                 185                 190
Gly Ser Leu Ser Ser Ala Arg Glu Ile Glu Asn Leu Pro Leu Arg Leu
            195                 200                 205
Phe Thr Leu Trp Arg Gly Pro Val Val Val Ala Ile Ser Leu Ala Thr
            210                 215                 220
Phe Phe Phe Leu Tyr Ser Phe Val Arg Asp Val Ile His Pro Tyr Ala
225                 230                 235                 240
Arg Asn Gln Gln Ser Asp Phe Tyr Lys Ile Pro Ile Glu Ile Val Asn
                245                 250                 255
Lys Thr Leu Pro Ile Val Ala Ile Thr Leu Leu Ser Leu Val Tyr Leu
                260                 265                 270
Ala Gly Leu Leu Ala Ala Ala Tyr Gln Leu Tyr Tyr Gly Thr Lys Tyr
            275                 280                 285
Arg Arg Phe Pro Pro Trp Leu Glu Thr Trp Leu Gln Cys Arg Lys Gln
     290                 295                 300
Leu Gly Leu Leu Ser Phe Phe Phe Ala Met Val His Val Ala Tyr Ser
305                 310                 315                 320
Leu Cys Leu Pro Met Arg Arg Ser Glu Arg Tyr Leu Phe Leu Asn Met
                325                 330                 335
Ala Tyr Gln Gln Val His Ala Asn Ile Glu Asn Ser Trp Asn Glu Glu
            340                 345                 350
Glu Val Trp Arg Ile Glu Met Tyr Ile Ser Phe Gly Ile Met Ser Leu
            355                 360                 365
Gly Leu Leu Ser Leu Leu Ala Val Thr Ser Ile Pro Ser Val Ser Asn
```

8

```
            370                          375                          380
Ala Leu Asn Trp Arg Glu Phe Ser Phe Ile Gln Ser Thr Leu Gly Tyr
385                          390                          395                          400
Val Ala Leu Leu Ile Ser Thr Phe His Val Leu Ile Tyr Gly Trp Lys
                      405                          410                          415
Arg Ala Phe Glu Glu Glu Tyr Tyr Arg Phe Tyr Thr Pro Pro Asn Phe
                      420                          425                          430
Val Leu Ala Leu Val Leu Pro Ser Ile Val Ile Leu Asp Leu Leu Gln
                      435                          440                          445
Leu Cys Arg Tyr Pro Asp
          450


<210> 7
<211> 4429
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (85)...(1464)

<400> 7
cgaaacttcc ctctacccgc ccggcccgcg gcgcgcaccg ttggcgctgg acgcttcctc         60
cttggaagcg cctctccctc agtt atg gag aaa act tgt ata gat gca ctt          111
                          Met Glu Lys Thr Cys Ile Asp Ala Leu
                            1                   5

cct ctt act atg aat tct tca gaa aag caa gag act gta tgt att ttt         159
Pro Leu Thr Met Asn Ser Ser Glu Lys Gln Glu Thr Val Cys Ile Phe
 10                  15                  20                  25

gga act ggt gat ttt gga aga tca ctg gga ttg aaa atg ctc cag tgt         207
Gly Thr Gly Asp Phe Gly Arg Ser Leu Gly Leu Lys Met Leu Gln Cys
                  30                  35                  40

ggt tat tct gtt gtt ttt gga agt cga aac ccc cag aag acc acc cta         255
Gly Tyr Ser Val Val Phe Gly Ser Arg Asn Pro Gln Lys Thr Thr Leu
              45                  50                  55

ctg ccc agt ggt gca gaa gtc ttg agc tat tca gaa gca gcc aag aag         303
Leu Pro Ser Gly Ala Glu Val Leu Ser Tyr Ser Glu Ala Ala Lys Lys
          60                  65                  70

tct ggc atc ata atc ata gca atc cac aga gag cat tat gat ttt ctc         351
Ser Gly Ile Ile Ile Ile Ala Ile His Arg Glu His Tyr Asp Phe Leu
          75                  80                  85

aca gaa tta act gag gtt ctc aat gga aaa ata ttg gta gac atc agc         399
Thr Glu Leu Thr Glu Val Leu Asn Gly Lys Ile Leu Val Asp Ile Ser
 90                  95                  100                 105

aac aac ctc aaa atc aat caa tat cca gaa tct aat gca gag tac ctt         447
Asn Asn Leu Lys Ile Asn Gln Tyr Pro Glu Ser Asn Ala Glu Tyr Leu
                  110                 115                 120

gct cat ttg gtg cca gga gcc cac gtg gta aaa gca ttt aac acc atc         495
Ala His Leu Val Pro Gly Ala His Val Val Lys Ala Phe Asn Thr Ile
```

9

```
tca gcc tgg gct ctc cag tca gga gca ctg gat gca agt cgg cag gtg        543
Ser Ala Trp Ala Leu Gln Ser Gly Ala Leu Asp Ala Ser Arg Gln Val
        140                 145                 150

ttt gtg tgt gga aat gac agc aaa gcc aag caa aga gtg atg gat att        591
Phe Val Cys Gly Asn Asp Ser Lys Ala Lys Gln Arg Val Met Asp Ile
    155                 160                 165

gtt cgt aat ctt gga ctt act cca atg gat caa gga tca ctc atg gca        639
Val Arg Asn Leu Gly Leu Thr Pro Met Asp Gln Gly Ser Leu Met Ala
170                 175                 180                 185

gcc aaa gaa att gaa aag tac ccc ctg cag cta ttt cca atg tgg agg        687
Ala Lys Glu Ile Glu Lys Tyr Pro Leu Gln Leu Phe Pro Met Trp Arg
                190                 195                 200

ttc ccc ttc tat ttg tct gct gtg ctg tgt gtc ttc ttg ttt ttc tat        735
Phe Pro Phe Tyr Leu Ser Ala Val Leu Cys Val Phe Leu Phe Phe Tyr
                205                 210                 215

tgt gtt ata aga gac gta atc tac cct tat gtt tat gaa aag aaa gat        783
Cys Val Ile Arg Asp Val Ile Tyr Pro Tyr Val Tyr Glu Lys Lys Asp
        220                 225                 230

aat aca ttt cgt atg gct att tcc att cca aat cgt atc ttt cca ata        831
Asn Thr Phe Arg Met Ala Ile Ser Ile Pro Asn Arg Ile Phe Pro Ile
    235                 240                 245

aca gca ctt aca ctg ctt gct ttg gtt tac ctc cct ggt gtt att gct        879
Thr Ala Leu Thr Leu Leu Ala Leu Val Tyr Leu Pro Gly Val Ile Ala
250                 255                 260                 265

gcc att cta caa ctg tac cga ggc aca aaa tac cgt cga ttc cca gac        927
Ala Ile Leu Gln Leu Tyr Arg Gly Thr Lys Tyr Arg Arg Phe Pro Asp
                270                 275                 280

tgg ctt gac cac tgg atg ctt tgc cga aag cag ctt ggc ttg gta gct        975
Trp Leu Asp His Trp Met Leu Cys Arg Lys Gln Leu Gly Leu Val Ala
                285                 290                 295

ctg gga ttt gcc ttc ctt cat gtc ctc tac aca ctt gtg att cct att       1023
Leu Gly Phe Ala Phe Leu His Val Leu Tyr Thr Leu Val Ile Pro Ile
                300                 305                 310

cga tat tat gta cga tgg aga ttg gga aac tta acc gtt acc cag gca       1071
Arg Tyr Tyr Val Arg Trp Arg Leu Gly Asn Leu Thr Val Thr Gln Ala
        315                 320                 325

ata ctc aag aag gag aat cca ttt agc acc tcc tca gcc tgg ctc agt       1119
Ile Leu Lys Lys Glu Asn Pro Phe Ser Thr Ser Ser Ala Trp Leu Ser
330                 335                 340                 345

gat tca tat gtg gct ttg gga ata ctt ggg ttt ttt ctg ttt gta ctc       1167
Asp Ser Tyr Val Ala Leu Gly Ile Leu Gly Phe Phe Leu Phe Val Leu
                350                 355                 360
```

10

```
ttg gga atc act tct ttg cca tct gtt agc aat gca gtc aac tgg aga        1215
Leu Gly Ile Thr Ser Leu Pro Ser Val Ser Asn Ala Val Asn Trp Arg
            365             370             375

gag ttc cga ttt gtc cag tcc aaa ctg ggt tat ttg acc ctg atc ttg        1263
Glu Phe Arg Phe Val Gln Ser Lys Leu Gly Tyr Leu Thr Leu Ile Leu
        380             385             390

tgt aca gcc cac acc ctg gtg tac ggt ggg aag aga ttc ctc agc cct        1311
Cys Thr Ala His Thr Leu Val Tyr Gly Gly Lys Arg Phe Leu Ser Pro
        395             400             405

tca aat ctc aga tgg tat ctt cct gca gcc tac gtg tta ggg ctt atc        1359
Ser Asn Leu Arg Trp Tyr Leu Pro Ala Ala Tyr Val Leu Gly Leu Ile
410             415             420             425

att cct tgc act gtg ctg gtg atc aag ttt gtc cta atc atg cca tgt        1407
Ile Pro Cys Thr Val Leu Val Ile Lys Phe Val Leu Ile Met Pro Cys
            430             435             440

gta gac aac acc ctt aca agg atc cgc cag ggc tgg gaa agg aac tca        1455
Val Asp Asn Thr Leu Thr Arg Ile Arg Gln Gly Trp Glu Arg Asn Ser
            445             450             455

aaa cac tag aaaaagcatt gaatggaaaa tcaatattta aaacaaagtt              1504
Lys His  *
```

```
caatttagct ggatttctga actatggttt tgaatgttta aagaagaatg atgggtacag        1564
ttaggaaagt ttttttctta caccgtgact gagggaaaca ttgcttgtct ttgagaaatt        1624
gactgacata ctggaagaga acaccatttt atctcaggtt agtgaagaat cagtgcaggt        1684
ccctgactct tattttccca gaggccatgg agctgagatt gagactagcc ttgtggtttc        1744
acactaaaga gtttccttgt tatgggcaac atgcatgacc taatgtcttg caaaatccaa        1804
tagaagtatt gcagcttcct tctctggctc aagggctgag ttaagtgaaa ggaaaaacag        1864
cacaatggtg accactgata aaggctttat taggtatatc tgaggaagtg ggtcacatga        1924
aatgtaaaaa gggaatgagg tttttgttgt tttttggaag taaaggcaaa cataaatatt        1984
accatgatga attctagtga aatgacccct tgactttgct tttcttaata cagatattta        2044
ctgagaggaa ctattttat aacacaagaa aaatttacaa ttgattaaaa gtatccatgt        2104
cttggataca tacgtatcta tagagctggc atgtaattct tcctctataa agaataggta        2164
taggaaagac tgaataaaaa tggagggata tccccttgga tttcacttgc attgtgcaat        2224
aagcaaagaa gggttgataa aagttcttga tcaaaaagtt caaagaaacc agaattttag        2284
acagcaagct aaataaatat tgtaaaattg cactatatta ggttaagtat tatttaggta        2344
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tttctcaaat ccttgctgaa atttaggatg gttctcactg tttttctgtg ctgatagtac        2644
cctttccaag gtgaccttca gggggattaa ccttcctagc tcaagcaatg agctaaaagg        2704
agccttatgc atgatcttcc cacatatcaa aataactaaa aggcactgag tttggcattt        2764
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tgacattata caaaaatgat taaaatatat taaaacaaca tcaacaatcc aggatatttt        2884
tctataaaac tttttaaaaa taattgtatc tatatattca attttacatc cttttttcaaa       2944
ggctttgttt ttctaaaggc tttgttttcc tttttattat ttttttcttt tttattttttt      3004
tgagacagtc ttgctctgtc gctcaggctg gagtgcagtg cacgatctc agctcactgc         3064
aacctcctcc tcccaggttc aagtgattct tgttcatcag cctcccgagt agctgggact        3124
acaggcatgt gccactatgc ccagctaatt tttgtacttt tagtagagac agggtttcac        3184
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11

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cacattggtc aggctggtct tgaaatgctg gcgtcaagtg atctgcctgc ctccgcctta    3244
cgtaatatat tttcttaatg gctgcataat atcacatcaa ataggcattt ttcaaacctc    3304
tttccttatt aaacatgtag actatatcca ttttttacta aaataaataa catttcagat    3364
aatatctttg cactgataat gttgccaagc catttctaaa gtgaccttat caatttaatt    3424
accattggat gagggtgttg ctttcatcgc accattgtag attgtctttt ttatttcaat    3484
ttgcgtttat ttataactgg ttgcaaaggt acacagaaca cacgctcctt caacttatct    3544
ttgataaacc caagcaagga tacaaaaagt tggacgacat tgagtagagt catggtatac    3604
ggtgctgacc ctacagtatc agtggaaaag ataaggaaaa tgtcactact cacctatgtt    3664
atgcaaaaca gttaggtgtg ctggggctgg atactgctct tttacttgag cattggttga    3724
ttaaagttta ggtaccatcc aggctggtct agagaagtct ttggagttaa ccatgctctt    3784
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aatgccatcc ataggtaaaa tgctgaccta tagaaaaaaa tgaactctac ttttatagcc    3904
tagtaaaaat gctctacctg agtagttaaa agcaattcat gaagcctgaa gctaaagagc    3964
actctgatgg ttttggcata atagctgcat ttccagacct gacctttggc cccaaccaca    4024
agtgctccaa gccccaccag ctgaccaaag aaagcccaag ttctccttct gtccttccca    4084
caacctccct gctcccaaaa ctatgaaatt aatttgacca tattaacaca gctgactcct    4144
ccagtttact taaggtagaa agaatgagtt tacaacagat gaaaataagt gctttgggcg    4204
aactgtattc cttttaacag atccaaacta ttttacattt aaaaaaaaag ttaaactaaa    4264
cttctttact gctgatatgt ttcctgtatt ctagaaaaat ttttacactt tcacattatt    4324
tttgtacact ttccccatgt taagggatga tggctttttat aaatgtgtat tcattaaatg    4384
ttactttaaa aataaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaa                     4429


<210> 8
<211> 459
<212> PRT
<213> Homo sapiens

<400> 8
Met Glu Lys Thr Cys Ile Asp Ala Leu Pro Leu Thr Met Asn Ser Ser
1               5                   10                  15
Glu Lys Gln Glu Thr Val Cys Ile Phe Gly Thr Gly Asp Phe Gly Arg
            20                  25                  30
Ser Leu Gly Leu Lys Met Leu Gln Cys Gly Tyr Ser Val Val Phe Gly
        35                  40                  45
Ser Arg Asn Pro Gln Lys Thr Thr Leu Leu Pro Ser Gly Ala Glu Val
    50                  55                  60
Leu Ser Tyr Ser Glu Ala Ala Lys Lys Ser Gly Ile Ile Ile Ile Ala
65                  70                  75                  80
Ile His Arg Glu His Tyr Asp Phe Leu Thr Glu Leu Thr Glu Val Leu
                85                  90                  95
Asn Gly Lys Ile Leu Val Asp Ile Ser Asn Asn Leu Lys Ile Asn Gln
            100                 105                 110
Tyr Pro Glu Ser Asn Ala Glu Tyr Leu Ala His Leu Val Pro Gly Ala
        115                 120                 125
His Val Val Lys Ala Phe Asn Thr Ile Ser Ala Trp Ala Leu Gln Ser
    130                 135                 140
Gly Ala Leu Asp Ala Ser Arg Gln Val Phe Val Cys Gly Asn Asp Ser
145                 150                 155                 160
Lys Ala Lys Gln Arg Val Met Asp Ile Val Arg Asn Leu Gly Leu Thr
                165                 170                 175
Pro Met Asp Gln Gly Ser Leu Met Ala Ala Lys Glu Ile Glu Lys Tyr
            180                 185                 190
Pro Leu Gln Leu Phe Pro Met Trp Arg Phe Pro Phe Tyr Leu Ser Ala
        195                 200                 205
Val Leu Cys Val Phe Leu Phe Phe Tyr Cys Val Ile Arg Asp Val Ile
    210                 215                 220
Tyr Pro Tyr Val Tyr Glu Lys Lys Asp Asn Thr Phe Arg Met Ala Ile
```

12

```
225                    230                    235                    240
Ser Ile Pro Asn Arg Ile Phe Pro Ile Thr Ala Leu Thr Leu Leu Ala
                 245                    250                    255
Leu Val Tyr Leu Pro Gly Val Ile Ala Ala Ile Leu Gln Leu Tyr Arg
             260                    265                    270
Gly Thr Lys Tyr Arg Arg Phe Pro Asp Trp Leu Asp His Trp Met Leu
         275                    280                    285
Cys Arg Lys Gln Leu Gly Leu Val Ala Leu Gly Phe Ala Phe Leu His
     290                    295                    300
Val Leu Tyr Thr Leu Val Ile Pro Ile Arg Tyr Tyr Val Arg Trp Arg
305                    310                    315                    320
Leu Gly Asn Leu Thr Val Thr Gln Ala Ile Leu Lys Lys Glu Asn Pro
                 325                    330                    335
Phe Ser Thr Ser Ser Ala Trp Leu Ser Asp Ser Tyr Val Ala Leu Gly
             340                    345                    350
Ile Leu Gly Phe Phe Leu Phe Val Leu Leu Gly Ile Thr Ser Leu Pro
             355                    360                    365
Ser Val Ser Asn Ala Val Asn Trp Arg Glu Phe Arg Phe Val Gln Ser
         370                    375                    380
Lys Leu Gly Tyr Leu Thr Leu Ile Leu Cys Thr Ala His Thr Leu Val
385                    390                    395                    400
Tyr Gly Gly Lys Arg Phe Leu Ser Pro Ser Asn Leu Arg Trp Tyr Leu
                 405                    410                    415
Pro Ala Ala Tyr Val Leu Gly Leu Ile Ile Pro Cys Thr Val Leu Val
             420                    425                    430
Ile Lys Phe Val Leu Ile Met Pro Cys Val Asp Asn Thr Leu Thr Arg
         435                    440                    445
Ile Arg Gln Gly Trp Glu Arg Asn Ser Lys His
     450                    455
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<210> 9
<211> 322
<212> DNA
<213> Homo sapiens

<400> 9
ggtcgacttt tcctttattc ctttgtcaga gatctgattc atccatatgc tagaaaccaa        60
cagagtgact tttacaaaat tcctatagag attgtgaata aaaccttacc tatagttgcc       120
attactttgc tctccctagt ataccttgca ggtcttctgg cagctgctta tcaactttat       180
tacggcacca agtataggag atttccacct tggttggaaa cctggttaca gtgtagaaaa       240
cagcttggat tactaagttg tttcttcgct atggtccatg ttgcctacag cctctgctta       300
ccgatgagaa ggtcagagag at                                                322

<210> 10
<211> 183
<212> DNA
<213> Homo sapiens

<400> 10
tttgcagctt tgcagatacc cagactgagc tggaactgga atttgtcttc ctattgactc        60
tacttcttta aaagcggctg cccattacat tcctcagctg tccttgcagt taggtgtaca       120
tgtgactgag tgttggccag tgagatgaag tctcctcaaa ggaaggcagc atgtgtcctt       180
ttt                                                                     183

<210> 11
<211> 448
<212> DNA
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<213> Homo sapiens

<400> 11
aagaaggaga atccatttag cacctcctca gcctggctca gtgattcata tgtggctttg   60
ggaatacttg ggttttttct gtttgtactc ttgggaatca cttctttgcc atctgttagc   120
aatgcagtca actggagaga gttccgattt gtccagtcca aactgggtta tttgaccctg   180
atcttgtgta cagcccacac cctggtgtac ggtgggaaga gattcctcag cccttcaaat   240
ctcagatggt atcttcctgc agcctacgtg ttagggctta tcattccttg cactgtgctg   300
gtgatcaagt ttgtcctaat catgccatgt gtagacaaca cccttacaag gatccgccag   360
ggctgggaaa ggaactcaaa acactagaaa aagcattgaa tggaaaatca atatttaaaa   420
caaagttcaa tttagctgga aaaaaaaa   448

<210> 12
<211> 401
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 11,56,233,250,310,326,377,398
<223> n=a, t, c, or g

<400> 12
ggccgcggca nccgctacga cctggtcaac ctggcagtca agcaggtctt ggccanacaa   60
gagccacctc tgggtgaagg aggaggtctg gcggatggag atctacctct ccctgggagt   120
gctggccctc ggcacgttgt ccctgctggc cgtgacctca ctgccgtcca ttgcaaactc   180
gctcaactgg agggagttca gcttcgttca gtcctcactg ggctttgtgg ccntcgtgct   240
gagcacactn cacacgctca cctacggctg acccgcgcc ttcgaggaga gccgctacaa   300
gttctacctn cctcccacct tcacgntcac gctgctggtg ccctgcgttc gttcatcctg   360
ggccaaagcc ctgtttntac tgccttgcat tcagccgnag a   401

<210> 13
<211> 133
<212> PRT
<213> Homo sapiens

<220>
<223> Xaa = Any amino acid

<400> 13
Ala Ala Ala Xaa Ala Thr Thr Trp Ser Thr Trp Gln Ser Ser Arg Ser
 1   5   10   15
Trp Pro Xaa Lys Ser His Leu Trp Val Lys Glu Glu Val Trp Arg Met
            20   25   30
Glu Ile Tyr Leu Ser Leu Gly Val Leu Ala Leu Gly Thr Leu Ser Leu
            35   40   45
Leu Ala Val Thr Ser Leu Pro Ser Ile Ala Asn Ser Leu Asn Trp Arg
    50   55   60
Glu Phe Ser Phe Val Gln Ser Ser Leu Gly Phe Val Ala Xaa Val Leu
65   70   75   80
Ser Thr Leu His Thr Leu Thr Tyr Gly Trp Thr Arg Ala Phe Glu Glu
                85   90   95
Ser Arg Tyr Lys Phe Tyr Leu Pro Pro Thr Phe Thr Xaa Thr Leu Leu
            100   105   110
Val Pro Cys Val Arg Ser Ser Trp Ala Lys Ala Leu Phe Xaa Leu Pro
            115   120   125
Cys Ile Gln Pro Xaa

                                    14

130

<210> 14
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 14
actttgttga tgaccaggat tgga   24

<210> 15
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 15
cagaacttca gcacacacag gaac   24

<210> 16
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 16
ttaggacaac ttgatcacca gca   23

<210> 17
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 17
tgtccagtcc aaactgggtt attt   24

<210> 18
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 18
agggagttca gcttcgttca gtc   23

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<210> 19
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 19
ggtagaactt gtagcggctc tcct                                              24

<210> 20
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 20
gactgagctg gaactggaat ttgt                                              24

<210> 21
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 21
tttgaggaga cttcatctca ctgg                                              24

<210> 22
<211> 14
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 22
ttttgtacaa gctt                                                         14

<210> 23
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> adaptor

<400> 23
ctaatacgac tcactatagg gctcgagcgg ccgcccgggc aggt                        44

<210> 24
<211> 10
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<212> DNA
<213> Artificial Sequence

<220>
<223> adaptor

<400> 24
ggcccgtcca   10

<210> 25
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> adaptor

<400> 25
gtaatacgac tcactatagg gcagcgtggt cgcggccgag gt   42

<210> 26
<211> 8
<212> DNA
<213> Artificial Sequence

<220>
<223> adaptor

<400> 26
cggctcca   8

<210> 27
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 27
ctaatacgac tcactatagg gc   22

<210> 28
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 28
tcgagcggcc gcccgggcag gt   22

<210> 29
<211> 20
<212> DNA
<213> Artificial Sequence

17

<220>
<223> primer

<400> 29
agcgtggtcg cggccgaggt   20

<210> 30
<211> 15
<212> PRT
<213> Homo sapiens

<400> 30
Tyr Gln Gln Val Gln Gln Asn Lys Glu Asp Ala Trp Ile Glu His
 1   5   10   15

<210> 31
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 31
gactgagctg gaactggaat ttgt   24

<210> 32
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 32
tttgaggaga cttcatctca ctgg   24
                                                                         /

<210> 33
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 33
acaagagcca cctctgggtg aa   22

<210> 34
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 34
agttgagcga gtttgcaatg gac